Figure 1

Stability Study of SAHH
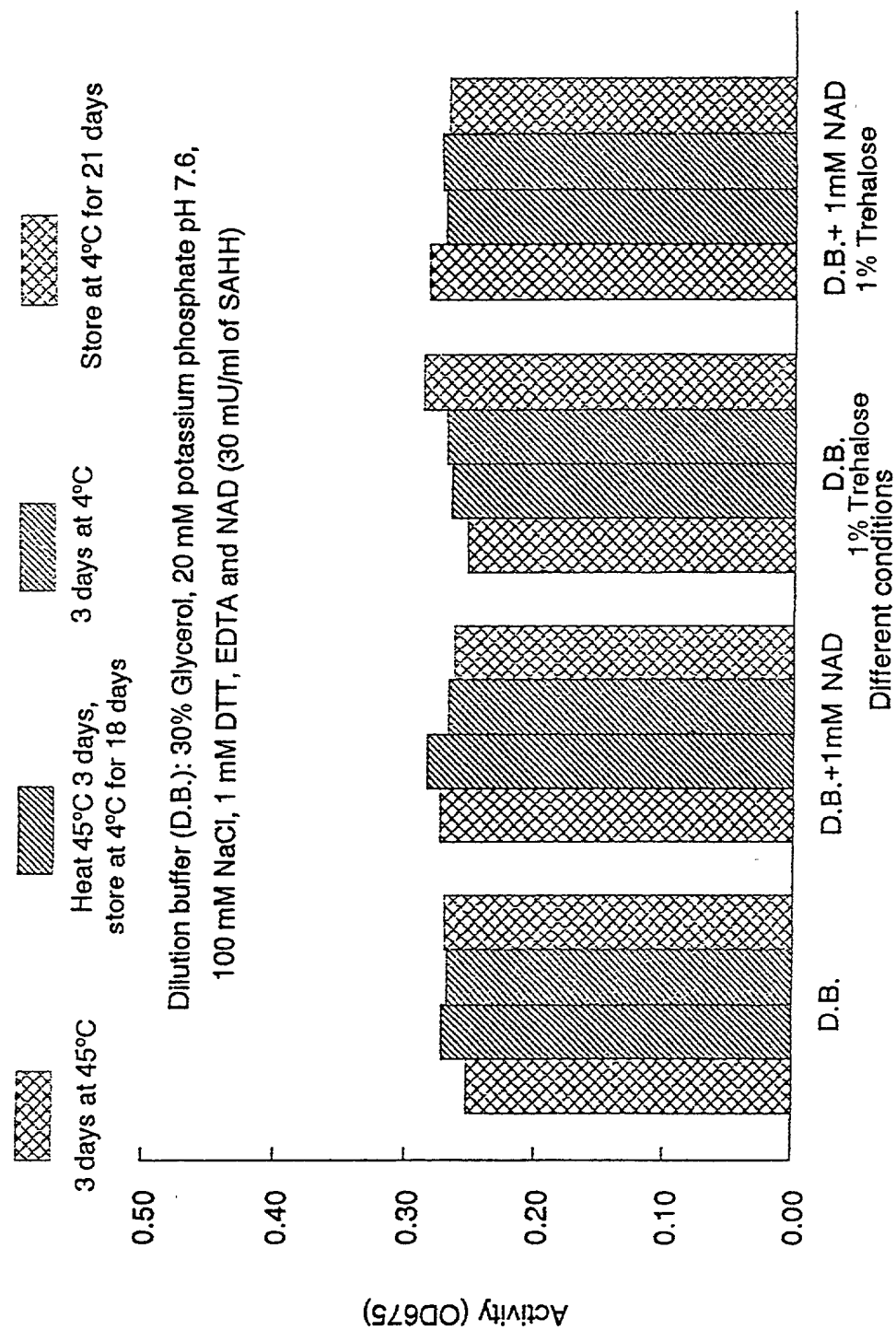
Heat 45°C 3 days,
store at 4°C for 18 days

3 days at 45°C

3 days at 4°C

Store at 4°C for 21 days

Dilution buffer (D.B.): 30% Glycerol, 20 mM potassium phosphate pH 7.6,
100 mM NaCl, 1 mM DTT, EDTA and NAD (30 mU/ml of SAHH)

D.B.

D.B.+1mM NAD

D.B.
1% Trehalose

D.B.+ 1mM NAD
1% Trehalose

Different conditions

Activity (OD675)

0.50   0.40   0.30   0.20   0.10   0.00

Figure 2

Screening of SAHH
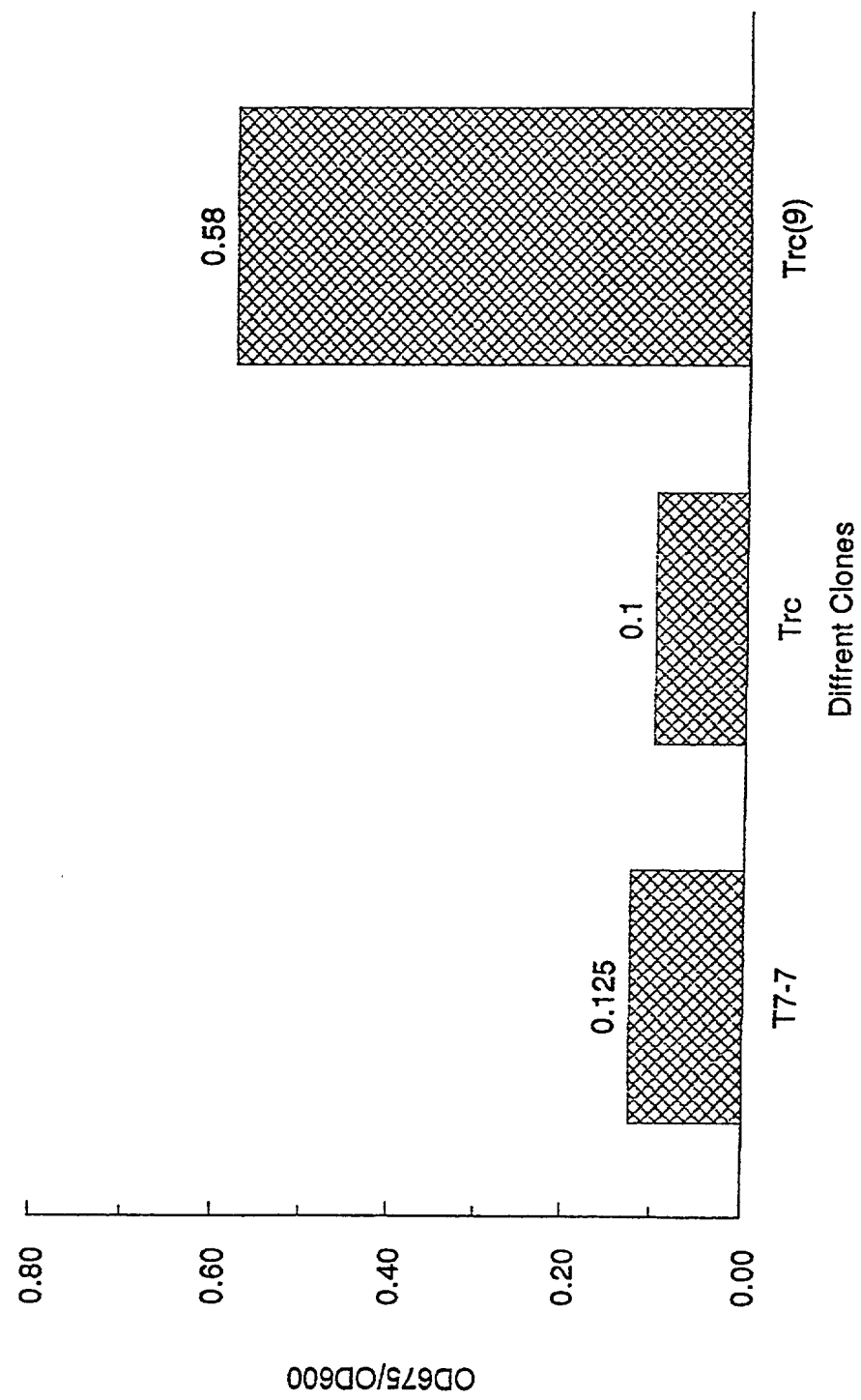
Figure 3
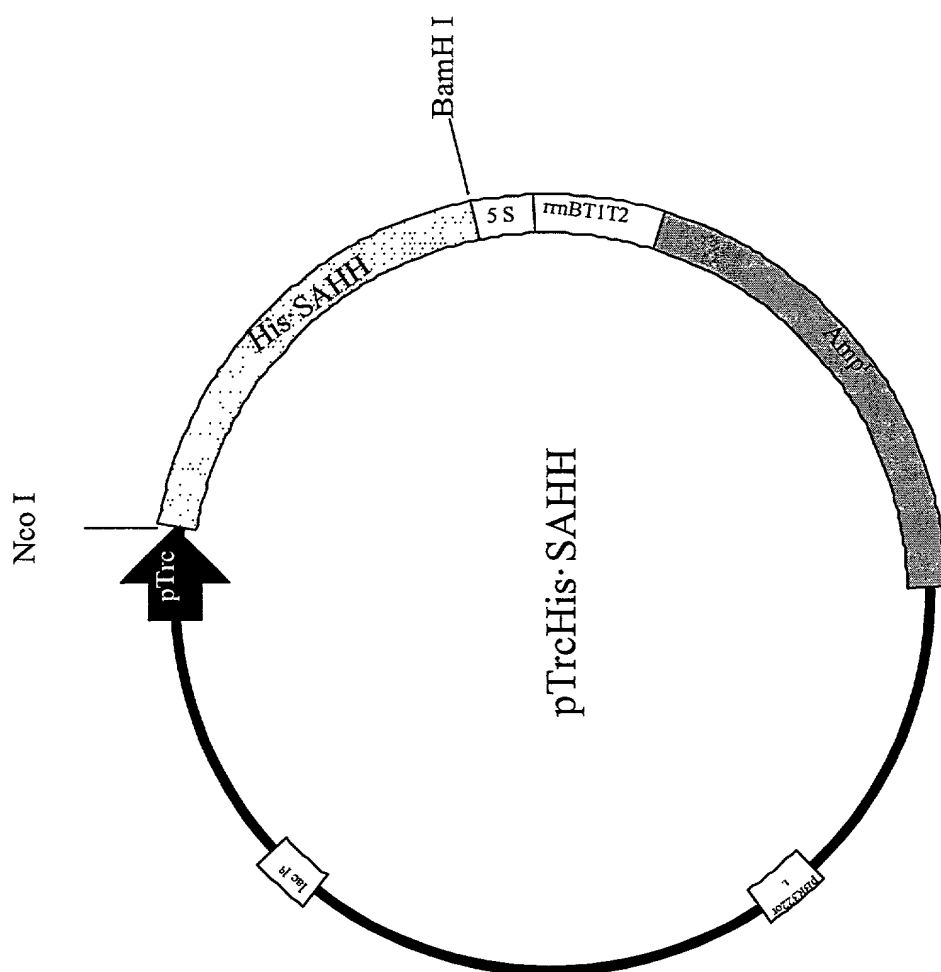
Figure 4

Stability of SAHH.His

3 days incubation in different temperature
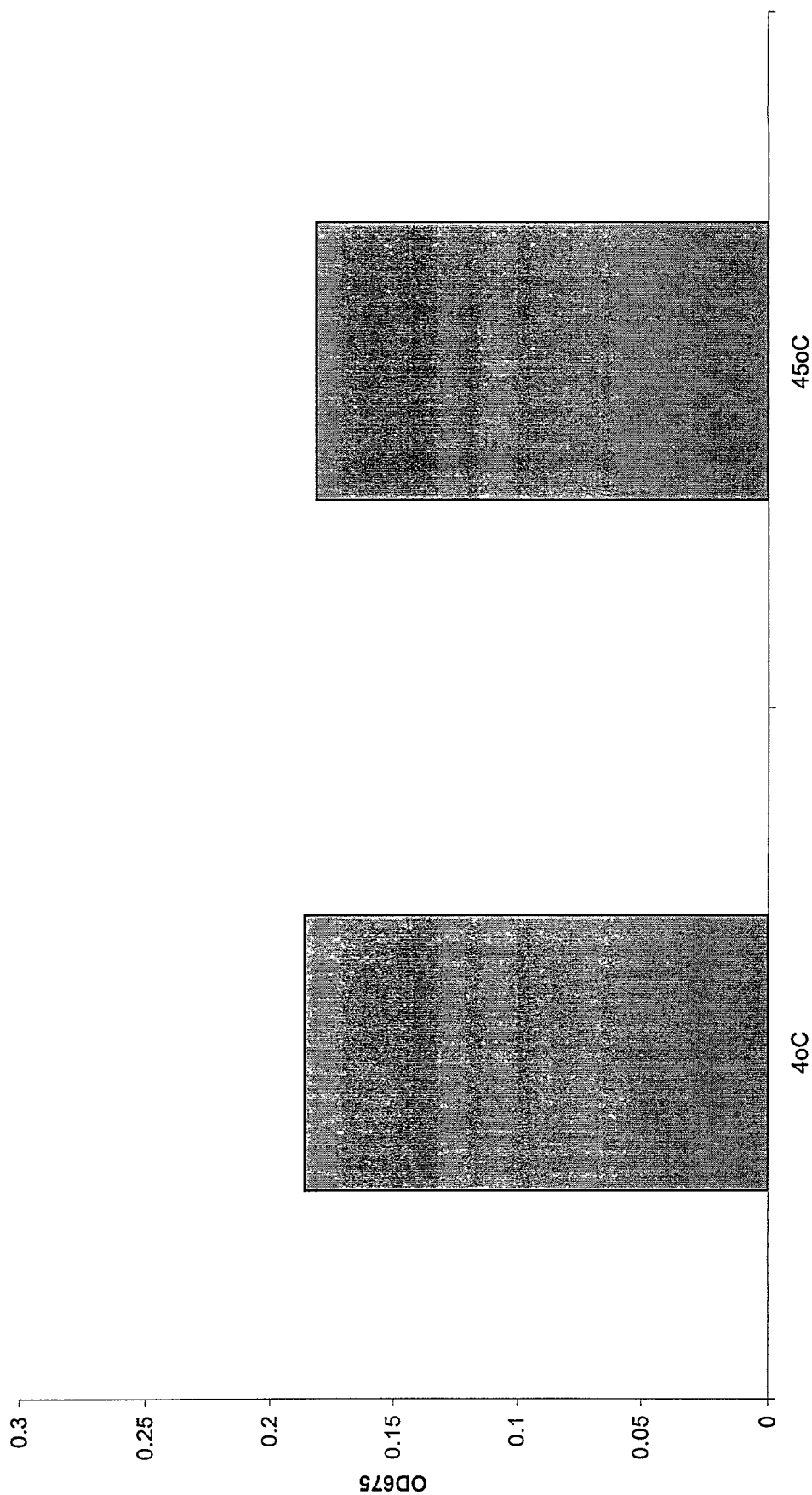
Figure 5

SIM - Results of the Alignment

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: Wild (1882 residues)
Sequence 2: A/C, (1594 residues)

using the parameters:

Number of alignments computed: 20
Cost of a matching aligned pair: 1
Cost of a transition: -1
Cost of a transversion: -1
Gap open penalty: 6.0
Gap extension penalty: 0.2

[handwritten annotations:]
Accession
GenBank.   U 40872
TVU - 40872 and
T vaginalis   A g111833 X
*   C*
dupos Feb
10/31/96
Baguara, A S F...
Mol Biochem Parant
(1996) 81 (-11

Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.
new.

99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

```
Wild    291 ATGGCTTGCAAATCACCTGCTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC
A/C,     71 ATGGCTTGCAAATCACCTACTGGTGCTCCATTCGAGTACAGAATTGCCGACATCAACCTC  SEQ ID NO.1
            ******************* ****************************************

Wild    351 CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
A/C,    131 CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
            ************************************************************

Wild    411 CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCAGAATCTCTGGTTCCCTC
```

Figure 6a

```
A/C,            191  CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCAGAATCTCTGGTTCCCTC
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            471  CACATGACAGTCCAGACAGCGGTCCTTATTGAGACACTCACAGCTCTTGGTGCTGATGTC
A/C,            251  CACATGACAGTCCAGACAGCCGTCCTCATCGAGACACTCACAGCTCTTGGTGCTGATGTC
                     * * * * * * * * * * * * * * * * * *   * * * * *   * *   * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            531  AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
A/C,            311  AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            591  GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
A/C,            371  GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            651  ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
A/C,            431  ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            711  CCACAGCAGGTTGTCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA
A/C,            491  CCACAGCAGGTTGTCGATGATGGTGGTGATGCTACACTCCTCATCTCCAAGGGCTTCGAA
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            771  TTCGAAACAGCCGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
A/C,            551  TTCGAAACAGCCGGTGCTGTTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
                     * * * * * * * * * * * * * * * * * *   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            831  GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT
A/C,            611  GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            891  GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC
A/C,            671  GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild            951  GAGAAGGAGGGCAAACTCCTCTTCCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
A/C,            731  GAGAAGGAGGGCAAACTCCTCTTCCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild           1011  AAGTTCGATAACATCTACGGCTGTCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
A/C,            791  AAGTTCGATAACATCTACGGCTGCCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
                     * * * * * * * * * * * * * * * * * * * * *   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild           1071  GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGGAAGGGC
A/C,            851  GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGCAAGGGC
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *   * * * * * *


Wild           1131  TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCTATC
A/C,            911  TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCAATC
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *   * * *


Wild           1191  TGCGCTCTCCAGGCTGTCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
A/C,            971  TGCGCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
                     * * * * * * * * * * * * * * * *   * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild           1251  GATGTCGATATCTTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
A/C,           1031  GATGTCGATATCTTCGTTACATGCACAGGAAACTGCGATATCATCTCTGTTGACATGATG
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild           1311  GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
A/C,           1091  GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
                     * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *


Wild           1371  ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC
```

Figure 6b

```
A/C,        1151 ACAGATGGCᴜᵢᵀCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC
                 ------*****************************************************

Wild        1431 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
A/C,        1211 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
                 ********************************************************----

Wild        1491 CTTGGTTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTCACAAACCAGACA
A/C,        1271 CTTGGCTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTCACAAACCAGACA
                 ***** ******************************************************

Wild        1551 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGATGAAGGTTTACACACTT
A/C,        1331 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGAAGAAGGTTTACACACTT
                 ******************************************* ****************

Wild        1611 CCGAAGCATCTCGATGAAGAAGTCGTTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT
A/C,        1391 CCGAAGCATCTCGATGAAGAAGTCGCTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT
                 ************************* **********************************

Wild        1671 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
A/C,        1451 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
                 ************************************************************

Wild        1731 TCTGATGCTTACCGTTATTAA
A/C,        1511 TCTGATGCTTACCGTTATTAA
                 *********************
```

65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

```
Wild         782 CGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACC
A/C,         682 CGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACC
                 ***** *   *  **** *****  ** ** * *** *    ****
```

80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild        1053 GGTATCAACCGTGCTTCCGA
A/C,         674 GGCATGAACGGTGTTTCCGA
                 ** ** *** *** ******
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild         564 GATACAGCCGCTGCTG
A/C,         554 GAAACAGCCGGTGCTG
                 ** ******* *****
```

64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild        1224 GTCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC
A/C,         710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACTCCTC
                 **** **** ** *  *   *** ***** * * *  ** **
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```
Wild         774 GAAACAGCCGGTGCTG
A/C,         344 GATACAGCCGCTGCTG
                 ** ******* *****
```

Figure 6c